

# final report

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## **Validation of genetic parameters for breeding *Bos indicus* cross cattle in the dry tropics**

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## PART I (For Public Release)

## 1. Abstract

Estimates of genetic parameters were made for Bos indicus cross genotypes in the dry tropics of northern Australia using data from Swan's Lagoon for 1981 to 1987. Analyses used a sire model and removed fixed effects for year, genotype, age of dam, time of birth and relevant interactions.

Results confirmed estimates of heritability from more benign environments for weights (0.20-0.36), post weaning growth (0.32 - 0.46), scrotal circumference (0.32) and temperament (0.08 - 0.70). Scrotal circumference was negatively genetically correlated with weight at 18 and 24 months and with post weaning growth (-0.23 to -0.71). Weight at weaning was negatively correlated with subsequent growth (-0.32 to -0.50). Other correlations were as expected.

These differences confirm the need for estimates of genetic parameters which are relevant to the extensive conditions and harsh environment of the dry tropics of northern Australia. Such relevant information needs to be incorporated into BREEDPLAN. The short duration (4 years), small number of sires (49) and incomplete data collection reduced the potential of this data set, but, in the context of the paucity of available data and cost of its collection, these data make a valuable contribution to our knowledge of genetic parameters for northern Australia. This project further illustrates the cost effectiveness of secondary use of existing data sets, and the enhancements to related projects from the statistical analyses done here.

## 2. Summary

The objectives of the project were to

- (a) Improve the efficiency of selection of Bos indicus cross cattle in the dry tropics of northern Australia.
- (b) Estimate genetic parameters for growth, fertility and adaptive traits of Bos indicus cross cattle in the dry tropics.
- (c) Contrast these estimates with published estimates from other environments so that the most appropriate estimates are available to beef producers in northern Australia.

The study was carried out at Swan's Lagoon Beef Cattle Research Station in the subcoastal spear grass region south of Townsville. Data from 485 animals in 4 cohorts of male progeny which remained intact to 24 months included liveweights, daily gains, scrotal circumference, sperm characteristics, temperament, tick resistance and buffalo fly resistance. Genetic parameters were estimated from a paternal half-sib model using a mixed model, least squares program for unequal subclass numbers. The important fixed effects were year, genotype, age of dam, time of birth and the interaction of year by genotype.

Heritability estimates were moderate (0.18 - 0.46) for liveweight and growth between weaning and 24 months, moderate for scrotal circumference at 24 months (0.32); low for move and temperament scores (0.08 - 0.23); and moderately high

for flight distance (0.32 - 0.70). The estimates were within the ranges reported in the literature. For instance, the estimates here agree with the average estimates in the literature for weaning weight (0.32 v 0.29) and gain from weaning to final weight (0.46 v 0.45) for Bos indicus cattle in tropical environments (Plasse, 1978). Hence, results found for Swan's Lagoon support heritability estimates from Belmont (Mackinnon, pers. comm.) and from tropical environments overseas.

Genetic correlations between weights at different ages were high (0.51 - 0.96) but weaning weight was negatively correlated with subsequent growth (-0.32 to -0.50). The correlations of scrotal circumference at 24 months and weight became increasingly negative with age while those with post-weaning growth were highly negative (-0.66 to -0.80). Temperament had genetic correlations with weight and post weaning growth which changed from positive at 6 months, to zero at 12 months and negative at 24 months. The correlations between weights validate the estimates from Belmont but the high negative correlation between weaning weight and subsequent growth is at variance with the zero correlation from Belmont (Mackinnon, pers.comm.). Similarly, the correlations of scrotal circumference with weights and growth differ from the high positive correlations found by Mackinnon (pers.comm.). These differences confirm the need for estimates of genetic parameters which are relevant to the extensive conditions and harsh environment of the dry tropics of northern Australia.

It is important that BREEDPLAN be relevant for northern Australia. For this to occur the current work to estimate genetic parameters from northern herds should be encouraged so that the most relevant estimates are used in BREEDPLAN.

The results presented here are derived from a small data set for which genetic analysis was only a secondary consideration during design and data collection. The short duration (4 years), small number of sires (49) and incomplete data collection reduced the potential of this data set, but, in the context of the paucity of available data and cost of its collection, these results make a valuable contribution to our knowledge of genetic parameters for northern Australia.

This project further illustrates the cost effectiveness of secondary use of existing data sets for statistical analysis and interpretation to glean additional information of relevance to the beef industry in northern Australia. The results of genetic analyses reported here represent only a small proportion of the effort and value derived from this data set. The preliminary steps of data collection, file establishment and validation, and statistical analysis of fixed effects models were necessary for the genetic analyses. However, statistical analysis enhanced and contributed substantially to the value, interpretation and presentation of related projects funded by AMLRDC. The major project here are the Swan's Lagoon genotype studies (DAQ44), temperament (UNQ7) and conception modelling (DAQ-NAP M9).

### 3. Recommendations

Genetic studies for the harsh environment of northern Australia are still needed to guide objective selection of superior breeding animals. Although estimates of heritability from more benign environments have been confirmed, there are important differences for genetic correlations which make extrapolation unwise.

Estimates of genetic parameters from northern herds need to be incorporated into BREEDPLAN to improve its applicability and acceptability to commercial producers in the dry tropics of northern Australia.

The secondary use of existing data sets to glean additional information of relevance to the beef industry can be extremely cost effective research.

## PART 2

### 1. Background and industry context

Bos indicus cattle and their crosses have been increasingly used in the tropical regions of northern Australia to the extent that they now form 78% of the cattle population in Queensland (Anon. 1989). The main productive advantages of the Bos indicus genotypes in the dry tropical environment are their greater drought and heat tolerance and increased resistance to internal and external parasitism, this being manifested primarily in a faster growth rate and lower mortality (Turner, 1975). In contrast, their reproductive performance has been described as sub-optimal (McClure, 1973), with the bull being recognised as a major contributor to this reduced herd reproductive performance (Entwistle, 1983).

Selection of genetically superior breeding stock is an important component of beef production. Livestock improvement depends on accurate and relevant estimates of the heritability of production traits as well as genetic and phenotypic correlations between these traits. Responses to selection may depend on the environment (Frisch and Vercoe, 1982; Baker and Morris, 1984). Therefore, estimates of genetic parameters derived from other environmental regions may not be applicable to all regions of northern Australia. There is a paucity of estimates for northern Australia so that it is important to use available data to improve and validate these estimates.

Direct selection based on estimates of genetic parameters for female fertility is inefficient because this is a sex limited trait. While selection among females is phenotypically effective, it does not allow for significant genetic improvement due to low heritability of most reproductive traits in females, low selection differentials and low replacement rates of breeding cows (Entwistle, 1983; Hammond and Graser, 1987). The majority of genetic improvement can be expected to come from use of superior sires since they transmit one half of their genetic composition to their progeny, and are responsible for the overall reproductive performance of the cows to which they are joined (Coulter and Foote, 1979). There are two possible strategies for sire selection for improving fertility in cows. The first is by early identification of superior sires through progeny testing, followed by direct selection. Since progeny testing of beef bulls for daughter fertility is impractical given the extensive nature of production in northern Australia, an alternative strategy is necessary. This involves indirect selection, where male traits are identified which are highly heritable and genetically correlated with other male traits and with fertility in females. Thus, reproductive and productive measures in males that will improve reproductive efficiency in both males and their female offspring need to be identified and described.

The study undertaken here provides estimates of genetic variation and correlation between growth, fertility and adaptive traits in intact males of four Bos indicus genotypes based on the Brahman and Sahiwal. Evidence of genetic antagonism across breeds between growth and adaptive traits (Frisch and Vercoe, 1984) can be checked for a wider range of genotypes and in a harsher environment. Results from this study, conducted at Swan's Lagoon, are compared and contrasted with those from a similar study at Belmont (Mackinnon, pers. comm.).

## 2. Objectives

The project aimed to:

- (a) Improve the efficiency of selection of Bos indicus cross cattle in the dry tropics of northern Australia.
- (b) Estimate genetic parameters for growth, fertility and adaptive traits of Bos indicus cross cattle in the dry tropics.
- (c) Contrast these estimates with published estimates from other environments so that the most appropriate estimates are available to beef producers in northern Australia.

In essence, the project set out to ensure that appropriate estimates of genetic parameters for use in objective selection of replacement animals are available for northern cattle breeders by either confirming the general applicability of current estimates or providing new ones. Thereby, the efficiency of selection and producer confidence in the relevance of objective selection will be improved for northern Australia.

## 3. Methodology

The study was carried out at Swan's Lagoon Beef Cattle Research Station, 100 km south of Townsville (latitude 20°05'S; longitude 147°14'E) in the subcoastal spear grass region of north Queensland. Average annual rainfall of 860 mm is markedly seasonal with 75% falling over the 4 months December to March. Principal native pasture species on the property are black spear grass (Heteropogon contortus), blue grasses (Bothriochloa spp. Dicanthium spp.), golden beard grass (Chrysopogon fallax) and kangaroo grass (Themeda triandra). These form an open woodland.

Commencing in 1967 four herds were developed from Shorthorn cows mated to Brahman and Sahiwal bulls, namely 1/2 Brahman, 1/2 Sahiwal, 3/4 Brahman and 3/4 Sahiwal. Inter se matings of these herds gave F2 et seq. generations, which were used in this study. Similar management practices were maintained for each herd with genotypes and offspring being run together to minimise environmental differences, except during mating periods. Mating commenced in late January and continued for 90 days in 24 single sire families of 25-35 cows each. Cows were checked 2-4 times weekly during the calving period to record birth dates. Branding was done in March-April and weaning in April-June, when calves were 5-7 months old. More complete information on property, genotypes and management has been given by Holroyd (1985).

Data from 485 animals in 4 male cohorts weaned from 1982 to 1985 which remained intact to 24 months were used. Liveweights were recorded at weaning, 12, 18 and 24 months and average daily gains calculated. Testicular and sperm characteristics were measured at 24 months as indicators of fertility. Scrotal circumference was measured and semen collected by electro ejaculation to determine percentages of motile spermatozoa and morphologically abnormal cells. A breeding soundness evaluation score (BSES) to provide an overall fertility score was calculated from these measurements. Temperament scores were assessed at 6, 12 and 24 months to give separate estimates for move score, temperament and flight distance as described by Fordyce (1985). Tick

resistance was assessed by artificial infestation and subsequent counting of engorging ticks. The number of buffalo flies was also counted.

Preliminary statistical analysis indentified the important fixed effects as year, genotype, age of dam, time of birth and the interaction of year by genotype. Heritability and genetic and phenotypic correlations were obtained from a mixed model with fixed effects as above and sires within genotypes as a random effect. This paternal half-sib relationship model was fitted using LSMLMW, a mixed model, least squares program for unequal subclass numbers (Harvey, 1987). Sires were used over 2 years where possible to prevent confounding of sires and years. Failed sires and those with less than 3 male offspring entire at 24 months were excluded from the analyses leaving a total of 49 sires over the 4 years and 4 genotypes of the study.

#### 4. Success in achieving objectives

The project used a sire model to successfully estimate heritability for weight, growth, scrotal circumference and temperament scores from weaning to 24 months of age. Genetic and phenotypic correlations between these traits were also estimated. Analysis done in collaboration with Dr D.L. Robinson, Animal Genetics and Breeding Unit, provided additional genetic information on growth, specifically for inclusion in BREEDPLAN to apply to Bos indicus genotypes in northern Australia. Our results have been compared with similar estimates from Belmont in central Queensland (Mackinnon, pers. comm.) to check on extrapolation from a less hostile environment.

The data set used in this project was collected primarily to evaluate 4 Bos indicus genotypes so that its suitability for genetic analysis was only a secondary consideration. Consequently, the data set was small in terms of genetic analysis (4 years and 49 sires) and data collection was incomplete. Tick count data had a negative sire component of variance which meant that heritability and genetic correlations could not be estimated. Buffalo fly counts and sperm characteristics had insufficient data for genetic analysis. Rectal temperatures were not measured. Low cell numbers and insufficient years of data prevented genetic analysis for female fertility. There were 3 years of data for 2 year old mating, 2 years for 3 year olds and 1 year for 4 year olds. However, in the context of the paucity of available data and cost of its collection, these results make a valuable contribution to our knowledge of genetic parameters for northern Australia.

#### 5. Findings and Conclusions

##### 5.1 Heritability estimates

Table 1 presents the estimates of heritability, sire and residual components of variance and means for the production traits of liveweight, growth, fertility and adaptation. Most estimates were low to moderate in value and had relatively low standard errors associated with them.

Heritability of liveweight was moderate in value (0.20 to 0.36) with the 24 months weight having the highest estimate. While variability between animals increased from weaning to 24 months, the variability between sires within genotypes was similar for weaning, 12 and 18 months but had doubled by 24 months.

Heritability of growth was low to moderate, with growth from 18 to 24 months having the lowest estimate (0.18) and growth from weaning to 24 months the highest estimate (0.46). Animal and sire variability was greatest in growth from 18 to 24 months, agreeing with the liveweight trend in variability at 24 months.

Estimates of heritability for scrotal circumference and scrotal circumference to age ratio were similar, and moderate in value. However the heritability estimate for scrotal circumference to weight ratio was high (0.94). Inclusion of the covariates age and weight at 24 months into the model explaining variability in scrotal circumference produced differing results. Addition of the age covariate was not significant ( $P > 0.05$ ) with resultant estimates of heritability ( $0.29 \pm 0.14$ ) and between sire and animal variability (0.45 and 5.79, respectively) being similar to the unadjusted scrotal circumference estimates. The inclusion of weight as a covariate was significant ( $P < 0.01$ ), with the heritability estimate being higher ( $0.68 \pm 0.18$ ), variability between sires being higher (0.86) and variability between animals being lower (4.20) than the unadjusted scrotal circumference estimates.

Heritability of temperament was generally low to moderate in value due to low variability between sires. Animal to animal variation was relatively consistent within a given temperament variable, reducing slightly with time. Low to moderate estimates of heritability were obtained for move score. Move score at 12 months had the highest heritability (0.23), having the largest variability between sires. In contrast, move score at 6 and 24 months had low heritabilities (0.10 and 0.11, respectively) due to the low and non-significant ( $P > 0.05$ ) variability between sires. Low estimates of heritability for temperament score were obtained as a consequence of low and non-significant ( $P > 0.05$ ) variability between sires. Moderate to high heritability values for flight distance were found, with flight distance at 24 months having the highest heritability (0.70), greatest variability between sires and least variability between animals.

No estimate of heritability for tick count could be obtained due to the negative estimate for the sire component of variance (see Table 1).

Mackinnon (pers.comm.) found similar estimates of heritability for liveweight at 6, 12 and 18 months at Belmont for the sire model and animal model including maternal genetic effects. However, her estimates were higher by .25 for the animal model, indicating that the maternal component inflated the environmental variance and that this component was ignored by the sire model. Maternal effects were not important for traits which occurred after weaning so that estimates of heritability for growth from 6-18 months were similar for sire and animal models and for the present study. Likewise Mackinnon's estimate for scrotal circumference agreed with the one for the present study.

## 5.2 Genetic and phenotypic correlations

Estimates of genetic and phenotypic correlations between liveweight, growth, fertility and adaptive traits are presented in this section. Correlations between liveweight and growth traits, between fertility traits and between adaptive traits are presented first. This is followed by correlations of liveweight and growth with fertility, liveweight and growth with adaptive traits, fertility with adaptive traits, and phenotypic correlations between sperm characteristics and the other parameters.



Table 2 lists the genetic and phenotypic correlations between liveweight and growth variables. The four liveweight variables were all highly genetically correlated with each other (0.51 to 0.96) and had associated small standard errors. Highest correlations were between weights at weaning and 12 months, 12 months and 18 months, and 18 months and 24 months with each having the same value  $0.96 \pm 0.07$ . Phenotypic correlations followed the genetic correlations closely. The three growth variables were all highly genetically correlated with each other (0.79 to 0.95). The phenotypic correlations followed the genetic correlations except for the relationship between growth from weaning to 18 months and 18 to 24 months where the value was zero. Genetic correlations between liveweight and growth traits changed with age. Correlations of weights at weaning, 12, 18 and 24 months with the three growth traits were moderate and negative, low and positive, moderate and positive, and high and positive (respectively) in value. Associated standard errors were moderate. Phenotypic correlations generally followed the genetic correlations, except for the relationships of 12 and 18 months weight to 18 to 24 months growth which were negative (-0.16 and -0.17, respectively). These correlations are similar to those found by Mackinnon (pers. comm.) at Belmont except that she found zero genetic correlation between weaning weight and subsequent growth to 18 months. The high negative correlation here indicates that animals compensated after weaning for inequalities in maternal environments prior to weaning.

The three scrotal circumference variables were all highly correlated with each other. Genetic correlations between scrotal circumference, scrotal circumference to age ratio and scrotal circumference to weight ratio were  $1.00 \pm 0.01$ ,  $0.77 \pm 0.15$  and  $0.81 \pm 0.17$ , in logical order. Phenotypic correlations were 0.99, 0.40 and 0.41, respectively.

Genetic and phenotypic correlations between temperament traits of males intact to 24 months are given in Table 3. Move score traits were all highly genetically correlated with each other, as were temperament score traits and flight distance traits. Moderate to high positive genetic correlations were obtained between move score and temperament score, move score and flight distance, and temperament score and flight distance. The exceptions were move score at 24 months with flight distance at 6 and 12 months (-0.44 and -0.49, respectively) and temperament score at 24 months with flight distance at 6 and 12 months (-0.54 and -0.66, respectively). Phenotypic correlations tended to follow the genetic correlations. However, they remained positive in value (0.17 to 0.21) when the genetic correlations were negative.

Table 4 lists the genetic and phenotypic correlations of scrotal circumference traits with the liveweight and growth traits of males intact to 24 months. The only positive genetic correlation was between scrotal circumference and weaning weight (0.29). The genetic correlations between scrotal circumference and liveweight became more negative with age. Highest negative genetic correlations were between scrotal circumference and growth traits (-0.66 to -0.80). Standard errors were moderate in value. The genetic correlations of scrotal circumference to age ratio with liveweight and growth were similar to those of scrotal circumference unadjusted, while those with scrotal circumference to weight ratio were all negative and larger in value. Phenotypic correlations of scrotal circumference and scrotal circumference to age ratio with liveweight and growth were low to moderate in value (0.11 to 0.45) while those of scrotal circumference to weight ratio ranged from -0.18 to -0.61 in value. These genetic correlations differ from those found by Mackinnon (pers. comm.) at Belmont where scrotal circumference at 18 months was

Table 2. Genetic (G) and phenotypic (P) correlations between liveweight and growth traits of males intact to 24 months.

		12 months	18 months	24 months	weaning to 18 months	18 to 24 months	weaning to 24 months
weaning	G	0.96 ± 0.07	0.75 ± 0.17	0.51 ± 0.23	-0.50 ± 0.34	-0.09 ± 0.42	-0.32 ± 0.32
	P	0.83	0.76	0.62	-0.09	-0.22	-0.23
12 months	G		0.96 ± 0.07	0.76 ± 0.15	0.17 ± 0.36	0.18 ± 0.47	0.00 ± 0.34
	P		0.86	0.76	0.28	-0.16	0.11
18 months	G			0.96 ± 0.07	0.21 ± 0.37	0.57 ± 0.54	0.39 ± 0.31
	P			0.88	0.58	-0.17	0.33
24 months	G				0.46 ± 0.25	0.79 ± 0.29	0.65 ± 0.17
	P				0.56	0.31	0.62
weaning to 18 months	G					0.79 ± 0.41	0.95 ± 0.07
	P					0.00	0.78
18 to 24 months	G						0.95 ± 0.17
	P						0.61

Table 3. Genetic (G) and phenotypic (P) correlations between temperament traits of males intact to 24 months.

	move score at		temperament score at		flight distance at		
	12 months	24 months	6 months	12 months	6 months	12 months	24 months
move score at 6 months	G	0.92 ± 0.36	1.07 ± 0.59	1.00 ± 0.05	0.86 ± 0.66	0.23 ± 0.46	1.05 ± 1.11
	P	0.52	0.36	0.95	0.37	0.23	0.22
12 months	G		0.56 ± 0.40	0.80 ± 0.28	0.53 ± 0.46	0.35 ± 0.32	0.69 ± 0.25
	P		0.51	0.54	0.54	0.26	0.27
24 months	G			0.89 ± 0.48	1.02 ± 0.07	-0.44 ± 0.43	0.18 ± 0.42
	P			0.37	0.95	0.20	0.18
temperament score at 6 months	G			0.92 ± 0.32	0.21 ± 0.40	0.32 ± 0.41	1.06 ± 0.60
	P			0.56	0.40	0.23	0.25
12 months	G			0.35 ± 0.66	0.42 ± 0.40	0.54 ± 0.40	0.86 ± 0.28
	P			0.57	0.25	0.29	0.28
24 months	G				-0.54 ± 0.50	-0.60 ± 0.54	0.22 ± 0.41
	P				0.21	0.19	0.22
flight distance at 6 months	G				0.98 ± 0.07		0.93 ± 0.11
	P				0.75		0.55
12 months	G						1.05 ± 0.08
	P						0.63

Table 4. Genetic (G) and phenotypic (P) correlations of scrotal circumference traits with liveweight and growth traits of males intact to 24 months.

		weaning weight	12 months	18 months	24 months	weaning to 18 months	18 to 24 months	weaning to 24 months
scrotal circumference	G	0.29 ± 0.31	-0.05 ± 0.38	-0.23 ± 0.37	-0.41 ± 0.27	-0.66 ± 0.27	-0.80 ± 0.37	-0.71 ± 0.23
	P	0.34	0.37	0.40	0.45	0.20	0.11	0.22
scrotal circumference to age ratio	G	0.26 ± 0.33	-0.09 ± 0.39	-0.30 ± 0.38	-0.46 ± 0.28	-0.70 ± 0.29	-0.80 ± 0.38	N.A.
	P	0.30	0.34	0.37	0.43	0.20	0.14	
scrotal circumference to liveweight ratio	G	-0.20 ± 0.27	-0.52 ± 0.33	-0.73 ± 0.34	-0.87 ± 0.28	-0.59 ± 0.28	-0.97 ± 0.35	N.A.
	P	-0.35	-0.45	-0.54	-0.61	-0.37	-0.18	

Table 5. Genetic (G) and phenotypic (P) correlations of temperament traits with liveweight and growth traits of males intact to 24 months

		weaning weight	12 months	18 months	24 months	weaning to 18 months	18 to 24 months	weaning to 24 months
move score at 6 months	G	0.93 ± 0.61	1.11 ± 0.71	1.07 ± 0.73	1.08 ± 0.63	0.05 ± 0.52	0.84 ± 0.71	0.40 ± 0.49
	P	0.00	-0.01	0.00	-0.01	0.00	0.00	-0.01
12 months	G	-0.04 ± 0.38	-0.02 ± 0.42	-0.10 ± 0.45	-0.04 ± 0.37	-0.06 ± 0.38	-0.06 ± 0.46	-0.02 ± 0.34
	P	-0.05	-0.04	-0.05	-0.09	-0.01	-0.07	-0.05
24 months	G	0.45 ± 0.51	0.42 ± 0.55	-0.06 ± 0.58	-0.21 ± 0.48	-0.74 ± 0.53	-0.47 ± 0.62	-0.65 ± 0.47
	P	-0.01	0.03	0.01	0.01	0.02	0.01	0.02
temperament score at 6 months	G	0.89 ± 0.46	1.10 ± 0.53	1.06 ± 0.56	0.94 ± 0.45	0.10 ± 0.45	0.43 ± 0.56	0.27 ± 0.41
	P	0.04	0.04	0.04	0.02	0.00	-0.02	-0.02
12 months	G	-0.06 ± 0.48	-0.03 ± 0.53	-0.11 ± 0.56	-0.04 ± 0.46	-0.06 ± 0.48	-0.02 ± 0.43	-0.09 ± 0.58
	P	-0.04	-0.03	-0.04	-0.07	0.00	-0.05	-0.04
24 months	G	0.36 ± 0.59	0.34 ± 0.63	-0.02 ± 0.66	-0.20 ± 0.54	-0.57 ± 0.60	-0.57 ± 0.73	-0.56 ± 0.55
	P	0.00	0.04	0.03	0.04	0.04	0.02	0.04
flight distance at 6 months	G	0.33 ± 0.31	0.31 ± 0.34	0.47 ± 0.36	0.42 ± 0.29	0.14 ± 0.32	0.14 ± 0.39	0.18 ± 0.28
	P	0.02	0.02	0.02	0.00	0.00	-0.05	-0.02
12 months	G	-0.03 ± 0.34	-0.02 ± 0.37	0.08 ± 0.39	-0.03 ± 0.33	0.20 ± 0.33	-0.38 ± 0.42	-0.01 ± 0.30
	P	-0.03	-0.03	0.00	-0.04	0.03	-0.09	-0.02
24 months	G	*	1.12 ± 1.51	0.44 ± 0.43	0.08 ± 0.34	*	-0.54 ± 0.37	-0.19 ± 0.36
	P	0.07	0.12	0.13	0.08	0.10	-0.10	0.02

\* Genetic correlation not estimated due to negative sire component of variance for weaning weight and growth from weaning to 18 months

highly correlated (0.62 to 0.73) with weights and growth between 6 and 18 months.

Estimates of genetic and phenotypic correlations of temperament variables with liveweight and growth are presented in Table 5. Similar trends in genetic correlation for move score and temperament score with liveweight variables were found, while flight distance behaved differently. Large standard errors were associated with all estimates. For move score and temperament score at 6 months, genetic correlations with liveweight were high (0.89 to 1.11), while for flight distance they ranged from 0.31 to 0.47. At 12 months genetic correlations of move score, temperament score and flight distance with the liveweight variables were all low (-0.11 to 0.08). For move score and temperament score at 24 months the correlations changed from moderate positive to moderate negative with age, while for flight distance the estimates declined with age. All phenotypic correlations were low with most effectively zero. Similar trends in genetic correlations for move score and temperament score with growth variables were found, with flight distance giving different results. Once again large standard errors were associated with these estimates. At 6 months genetic correlations of move score and temperament score with growth traits ranged from 0.05 to 0.84 but for flight distances were consistently low (0.14 to 0.18). At 12 months genetic correlations were low (-0.09 to -0.02) for move score and temperament score but ranged from -0.38 to 0.20 for flight distance. All three temperament variables had high negative genetic correlations at 24 months, except for the relationship between flight distance and growth from weaning to 24 months, which was -0.19. All phenotypic correlations were either side of and close to zero.

Table 6 presents the genetic and phenotypic correlations of temperament traits with scrotal circumference traits. Move score and temperament score had similar relationships with scrotal circumference while flight distance responded differently. Move score and temperament score at 6, 12 and 24 months had moderate to large and positive genetic correlations with all scrotal circumference variables. The exceptions were move score and temperament score at 6 months which had negative estimates (-0.24 and -0.18, respectively) with scrotal circumference to weight ratio. Negative genetic correlations (-0.11 to -0.27) were obtained between flight distance at 6 months and the scrotal circumference variables, while low correlations (0.02 to 0.18) were obtained at 12 and 24 months. All standard errors were moderate to large in value. Phenotypic correlations were low and near zero (0.00 to 0.15).

Phenotypic correlations within sperm characteristics, and of sperm characteristics with scrotal circumference and various liveweight and growth traits are presented in Table 7. The phenotypic correlation between % motility and % normal was moderate and positive in value. The relationships of scrotal circumference with % motility and % normal were basically zero BSES had high positive phenotypic correlations with its components; a moderate and positive phenotypic correlation with liveweight at 24 months; and no relationship with growth from weaning to 24 months and 18 to 24 months. Relationships between % motility and % normal with liveweight and growth were all low and close to zero, except for that between % normal and liveweight at 24 months whose value was 0.16.

**Table 6. Genetic (G) and phenotypic (P) correlations of temperament traits with scrotal circumference traits for males intact to 24 months.**

		unadjusted	scrotal circumference to age ratio	to liveweight ratio
move score at 6 months	G	0.82 ± 0.56	0.94 ± 0.62	-0.24 ± 0.40
	P	0.06	0.05	0.06
12 months	G	0.84 ± 0.34	0.94 ± 0.36	0.50 ± 0.26
	P	0.07	0.07	0.15
24 months	G	0.60 ± 0.51	0.63 ± 0.54	0.40 ± 0.39
	P	0.03	0.04	0.03
temperament score at 6 months	G	0.72 ± 0.43	0.81 ± 0.46	-0.18 ± 0.34
	P	0.09	0.09	0.06
12 months	G	1.04 ± 0.51	1.19 ± 0.56	0.62 ± 0.36
	P	0.06	0.07	0.12
24 months	G	0.54 ± 0.60	0.59 ± 0.64	0.39 ± 0.46
	P	0.03	0.04	0.01
flight distance at 6 months	G	-0.13 ± 0.31	-0.11 ± 0.34	-0.27 ± 0.24
	P	0.02	0.01	0.02
12 months	G	0.02 ± 0.34	0.03 ± 0.36	0.09 ± 0.26
	P	0.03	0.02	0.07
24 months	G	0.17 ± 0.32	0.18 ± 0.34	0.05 ± 0.27
	P	0.13	0.13	0.00

Table 7. Phenotypic correlations between sperm characteristics and various production traits for males intact to 24 months

	% Motility	% Normal	BSES
% motility		0.32	0.58
% normal			0.77
scrotal circumference	0.06	0.08	0.44
liveweight at 24 months	-0.02	0.16	0.22
growth from weaning to 24 months	-0.03	0.06	-0.05
growth from 18 to 24 months	-0.01	-0.02	-0.08



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## 6. Progress in commercialisation

Results from genetic analyses, particularly for growth parameters, are being incorporated into BREEDPLAN to improve its applicability and acceptability to commercial producers in the dry tropics of northern Australia. A critical element here is extending the period for evaluation of growth from 18 to 30 months to fit more closely with management practices in the north. The second extension adds confidence to the estimates of genetic parameters used in BREEDPLAN for extrapolation to northern Australia.

Further commercialisation and extension of results for bull selection on liveweight, growth, fertility and adaptive traits will flow on to producers from the normal advisory functions of QDPI and Agricultural Business Research Institute. The specific outcome of this project will be publication in a scientific journal.

## 7. Total funding and AMLRDC contribution

	1987-88	1988-89	1989-90	Total
QDPI	26,000	26,000	10,000	62,000
AGBU	-	-	10,000	10,000
AMLRDC	13,300	14,380	-	27,680

Contributions from QDPI and AGBU are estimates and are predominantly for salaries of staff working on the project. Not included here are costs associated with field data collection and herd management which was financed by QDPI and AMRC under project DAQ44, prior to the present project.

## 8. Impact on meat and livestock industry

The major impact of this project will be through BREEDPLAN and to a lesser extent, through extension and advisory services of QDPI. Estimates of genetic parameters will be based on data from Bos indicus cross cattle in harsher tropical environments incorporated with parameters for Bos taurus cattle in temperate environments and for Bos indicus cross in less stressful tropical environments. Efficient, objective identification of genetically superior animals within and across herds, especially stud herds, will permit their widespread use by industry.

Although this data set does contribute extra genetic information for the dry tropics of northern Australia, there remains a paucity of relevant genetic information for this environment. Extra data sets or more advanced statistical techniques could add to this pool of information within the next 5 years. Greater promotion and adoption of objective selection, for instance using BREEDPLAN, will increase the impact of results from this and related studies on the meat and livestock industry within the next 5 years.

## 9. Conclusions and recommendations

Although this study confirms estimates for heritability of growth and adaptive traits, it also identifies differences in genetic correlations between some traits. The major differences are negative genetic correlations for scrotal circumference at 24 months with weights at 18 and 24 months and growth post weaning, and for weaning weight with subsequent growth. These differences confirm the need for estimates of genetic parameters which are relevant to the extensive conditions and harsh environment of the dry tropics of northern Australia.

It is important that BREEDPLAN be relevant for northern Australia. For this to occur the current work to estimate genetic parameters from northern herds should be encouraged so that the most relevant estimates are used in BREEDPLAN.

The results presented here are derived from a small data set for which genetic analysis was only a secondary consideration during design and data collection. The short duration (4 years), small number of sires (49) and incomplete data collection reduced the potential of this data set, but, in the context of the paucity of available data and cost of its collection, these results make a valuable contribution to our knowledge of genetic parameters for northern Australia.

This project further illustrates the cost effectiveness of secondary use of existing data sets for statistical analysis and interpretation to glean additional information of relevance to the beef industry in northern Australia. The results of genetic analyses reported here represent only a small proportion of the effort and value derived from this data set. The preliminary steps of data collection, file establishment and validation, and statistical analysis of fixed effects models were necessary for genetic analyses. However, statistical analysis enhanced and contributed substantially to the value, interpretation and presentation of related projects funded by AMLRDC. The major projects here are the Swan's Lagoon genotype studies (DAQ44), temperament (UNQ7) and conception modelling (DAQ.NAP M9).